

We claim:

1. A process for determining the status of a living organism, comprising the steps of:
  - (a) sampling cellular material which contains at least a first microtubule, a second microtubule, and a multiplicity of microtubule associated proteins disposed between said first microtubule and said second microtubule,
  - (b) imaging said first microtubule, said second microtubule, and said multiplicity of microtubule associated proteins disposed between said first microtubule and said second microtubule,
  - (d) determining the positions of said first microtubule, said second microtubule, and said multiplicity of microtubule associated proteins disposed between said first microtubule and said second microtubule,
  - (e) determining the pattern of said microtubule associated proteins disposed between said first microtubule and said second microtubule,
  - (f) comparing the positions said first microtubule, said second microtubule, and said multiplicity of microtubule associated proteins disposed between said first microtubule and said second microtubule, with historic phenotypic data, and
  - (f) comparing the pattern of said microtubule associated proteins disposed between said first microtubule and said second microtubule with historic phenotypic data.
2. The process as recited in claim 1, wherein said positions of said first microtubule, said second microtubule, and said multiplicity of microtubule associated proteins disposed between said first microtubule is determined by X-ray crystallography.
3. The process as recited in claim 1, further comprising the step of determining the rates at which said multiplicity of microtubule associated proteins change said positions.

4. The process as recited in claim 1, further comprising the step of determining the composition of said microtubule associated proteins.
5. The process as recited in claim 4, wherein said compositions of said microtubule associated proteins are determined by protein isolation.
6. The process as recited in claim 4, wherein said compositions of said microtubule associated proteins are determined by mass spectrometry.
7. The process as recited in claim 1, further comprising the step of determining the Qbit pattern of the tubulin conformation state, wherein said first microtubule and said said second microtubule is each comprised of said tubulin.
8. The process as recited in claim 1, further comprising determining the speeds of microtubule-assisted protein transport of protein secondary messengers.
9. The process as recited in claim 1, further comprising determining the destinations of microtubule assisted protein transport of protein secondary messengers.
10. The process as recited in claim 1, further comprising adhering said sampled cells to a solid support.
11. The process as recited in claim 10, wherein said solid support is comprised of polystyrene.
12. The process as recited in claim 1, wherein said sampled cells are isolated and maintained as single cells.
13. The process as recited in claim 1, wherein said multiplicity of microtubule associated proteins are imaged by slow neutron imaging.
14. The process as recited in claim 1, further comprising the step of digitizing data produced by said imaging said first microtubule, said second microtubule, and said multiplicity of

microtubule associated proteins disposed between said first microtubule, thereby producing digitized data.

15. The process as recited in claim 14, further comprising the step of electronically manipulating said digitized data.

15. The process as recited in claim 14, further comprising the step of analyzing said digitized data.

16. The process as recited in claim 1, further comprising the step of treating said living organism.

17. The process as recited in claim 16, wherein said living organism is treated by the application of external electromagnetic energy.

18. The process as recited in claim 16, wherein said living organism is treated with coherent phonon energy.

19. The process as recited in claim 16, further comprising the step of changing the attachment pattern of said microtubule associated proteins.

20. The process as recited in claim 16, further comprising the step of changing the amino acid sequence of individual microtubule associated proteins.

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